

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:23:18 : Search time 39.0266 Seconds

(without alignments)  
3273.388 Million cell updates/sec

Title: US-10-054-680-4

Sequence: 1 MAWLRIQPLTSAFLHFGVLTVT.....ADYGRGCGEDSRDGRASIG 620

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Search: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3093	95.8	924	4	Q96G01
2	3093	95.8	924	4	Q96G02
3	3012	93.3	595	11	Q9EP08
4	3012	93.3	928	11	Q9EPU8
5	2157	66.8	934	6	Q97801
6	2156.5	66.8	941	6	Q28662
7	2154.5	66.7	602	6	Q9TV05
8	2136.5	66.2	941	6	Q9TS14
9	2133	66.1	934	11	Q9R238
10	2131	66.0	934	11	Q9WU30
11	2129	65.9	957	11	Q9R239
12	2128.5	65.9	600	11	Q91ZJ7
13	2126.5	65.8	600	11	Q9ET74
14	2124	65.8	962	11	Q924Y2
15	2124	65.8	969	11	Q9WU29
16	2102	65.1	583	13	Q91850

17	2099.5	65.0	940	11	Q35157	035157 mus musculu
18	2030	62.9	968	13	Q9PT19	09pt19 oncorhynch
19	1501	46.5	892	5	Q02196	002196 loligo opal
20	1339.5	41.5	950	5	Q24413	024413 drosophila
21	1339.5	41.5	950	5	Q9VD55	09vd55 drosophila
22	1328	41.1	950	5	Q18367	018367 drosophila
23	1288	39.9	925	5	Q45630	045630 caenorhabd1
24	1285.5	39.8	925	5	Q94161	094161 caenorhabd1
25	1278	39.6	254	13	Q9YH83	09yh83 gallus gall
26	1278	39.6	793	4	Q9H021	09h021 homo sapien
27	1160	35.9	880	5	Q21609	021609 caenorhabd1
28	1105.5	34.2	263	13	Q9YGE0	09yge0 oncorhynch
29	1046.5	32.4	263	13	Q9YH84	09yh84 gallus gall
30	1038	32.2	264	13	Q9YGE1	09yge1 oncorhynch
31	970.5	30.1	267	13	Q9YGE2	09yge2 oncorhynch
32	660	20.4	199	11	Q8R505	08r505 mus musculu
33	655	20.3	860	13	Q91849	091849 xenopus lae
34	633.5	19.6	807	5	Q21895	021895 caenorhabd1
35	523.5	16.2	171	11	Q8R504	08r504 mus musculu
36	519	16.1	215	11	Q9Z0T8	09z0t8 ratus norv
37	487	15.1	158	6	Q9MY54	09my54 oryctolagus
38	481	14.9	92	11	Q8R503	08r503 mus musculu
39	362.5	11.2	539	10	Q22252	022252 arabidopsis
40	291	9.0	263	5	Q8WPE2	08wpe2 porcellio s
41	222	6.9	1130	11	Q91WD8	091wd8 mus musculu
42	205	6.4	1014	6	Q62805	062805 tursiops tr
43	202	6.3	6307	4	Q8WXC9	08wxc9 homo sapien
44	200	6.2	652	5	Q8T8P0	08t8p0 strongyloce
45	187	5.8	4936	16	Q8YKJ3	08ykj3 anabaena sp

# ALIGNMENTS

RESULT 1	Q96G01	PRELIMINARY:	PRT:	924 AA.
ID	Q96G01			
AC	Q96G01			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			
DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)			
DE	01-JUN-2002 (TREMBlrel. 21, Last annotation update)			
DE	Sodium/calcium exchanger SCL8A3.			
GN	SCL8A3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	Bortoluzzi S.;			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Gabelini N.;			
RT	*Characterization of the human SCL8A3 gene for solute carrier family			
RT	8, member 3 (sodium/calcium exchanger).;			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ304853; CAC40985.1;			
DR	EMBL; AJ304853; CAC40985.1;			
DR	InterPro; IPR003644; Calx_beta.			
DR	InterPro; IPR004837; NaCa_Exmemb.			
DR	InterPro; IPR004836; Na_Ca_Ex.			
DR	Pfam; PF03160; Calx_beta; 2.			
DR	Pfam; PF01699; Na_Ca_Ex; 2.			
DR	TIGRFAMs; TIGR00845; Caca; 1.			
DR	TIGRFAMs; TIGR00845; Caca; 1.			
SO	SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;			
Query Match	95.8%; Score 3093; DB 4; Length 924;			
Best Local Similarity	100.0%; Pred. No. 3.2e-242;			
Matches	595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MAWLRIQPLTSAFLHFGVLTVFLNGLRARAGSGDVPSTGQNNESCGSSDCKEYIL 60			
DB	1 MAWLRIQPLTSAFLHFGVLTVFLNGLRARAGSGDVPSTGQNNESCGSSDCKEYIL 60			

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OY 61 PIWYPENPSLGDKIARIYIVFVALLIYMFVLSIIADRFMAIEVITSOBERVYTIKKPNC 120
DB 61 PIWYPENPSLGDKIARIYIVFVALLIYMFVLSIIADRFMAIEVITSOBERVYTIKKPNC 120
OY 121 TSTTTIRVNNENYVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGSPSTVGSAAFNMT 180
DB 121 TSTTTIRVNNENYVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGSPSTVGSAAFNMT 180
OY 181 ITGICVYVPDGETRKIKLRVFEFTAAWSIFAYIMYLILAFSPGVQVWEGLLTLFF 240
DB 181 ITGICVYVPDGETRKIKLRVFEFTAAWSIFAYIMYLILAFSPGVQVWEGLLTLFF 240
OY 241 FPVCVLLAVAVADKRLLEFYVMHKKRYTDKHKRGIIETEDHPKGIEMDKMNSHFLDGN 300
DB 241 FPVCVLLAVAVADKRLLEFYVMHKKRYTDKHKRGIIETEDHPKGIEMDKMNSHFLDGN 300
OY 301 LVPLEKEVDESREMRIRLKLKQKHPKDLQVLVEMANYALSHQOKSRAFYRIQATR 360
DB 301 LVPLEKEVDESREMRIRLKLKQKHPKDLQVLVEMANYALSHQOKSRAFYRIQATR 360
OY 361 MMTGAGNIIKHAABQAKKASSMSEVHTDEPDEFTSKVFEDPCSYQCLNCGAVLLTVVR 420
DB 361 MMTGAGNIIKHAABQAKKASSMSEVHTDEPDEFTSKVFEDPCSYQCLNCGAVLLTVVR 420
OY 421 KGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETOKEFVSGIIDDIFEEDEF 480
DB 421 KGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETOKEFVSGIIDDIFEEDEF 480
OY 481 FVRLSVNRLEEBOPEBGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTH 540
DB 481 FVRLSVNRLEEBOPEBGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTH 540
OY 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595
DB 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595

RESULT 2
O96OG2 PRELIMINARY: PRT: 925 AA.
AC O96OG2: 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabelini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304852; CAC40984.1; -.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Ext.
DR InterPro: IPR004836; NaCa_Ext.
DR Pfam; PF03160; Calx_beta; 2.
DR Pfam; PF01699; NaCa_Ext; 1.
DR TIGRFAMs; TIGR00845; caca; 1.
SQ SEQUENCE 925 AA; 102803 MW; OCCF8DA0881C4FDA CRC64;
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Query Match 95.8%; Score 3093; DB 4; Length 925;  
Best Local Similarity 100.0%; Pred. No. 3.2e-242;  
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MAMLRLOPLTSAFLHGLVTFVFLNLGLRAEAGSGDVPSTGONNESCSSGSDCKEGLV 60
DB 1 MAMLRLOPLTSAFLHGLVTFVFLNLGLRAEAGSGDVPSTGONNESCSSGSDCKEGLV 60
OY 61 PIWYPENPSLGDKIARIYIVFVALLIYMFVLSIIADRFMAIEVITSOBERVYTIKKPNC 120
DB 61 PIWYPENPSLGDKIARIYIVFVALLIYMFVLSIIADRFMAIEVITSOBERVYTIKKPNC 120
OY 121 TSTTTIRVNNENYVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGSPSTVGSAAFNMT 180
DB 121 TSTTTIRVNNENYVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGSPSTVGSAAFNMT 180
OY 181 ITGICVYVPDGETRKIKLRVFEFTAAWSIFAYIMYLILAFSPGVQVWEGLLTLFF 240
DB 181 ITGICVYVPDGETRKIKLRVFEFTAAWSIFAYIMYLILAFSPGVQVWEGLLTLFF 240
OY 241 FPVCVLLAVAVADKRLLEFYVMHKKRYTDKHKRGIIETEDHPKGIEMDKMNSHFLDGN 300
DB 241 FPVCVLLAVAVADKRLLEFYVMHKKRYTDKHKRGIIETEDHPKGIEMDKMNSHFLDGN 300
OY 301 LVPLEKEVDESREMRIRLKLKQKHPKDLQVLVEMANYALSHQOKSRAFYRIQATR 360
DB 301 LVPLEKEVDESREMRIRLKLKQKHPKDLQVLVEMANYALSHQOKSRAFYRIQATR 360
OY 361 MMTGAGNIIKHAABQAKKASSMSEVHTDEPDEFTSKVFEDPCSYQCLNCGAVLLTVVR 420
DB 361 MMTGAGNIIKHAABQAKKASSMSEVHTDEPDEFTSKVFEDPCSYQCLNCGAVLLTVVR 420
OY 421 KGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETOKEFVSGIIDDIFEEDEF 480
DB 421 KGDMSKTMVVDYKTEDEGSANAGADYEFTGTVLKPGETOKEFVSGIIDDIFEEDEF 480
OY 481 FVRLSVNRLEEBOPEBGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTH 540
DB 481 FVRLSVNRLEEBOPEBGMPAIFNSLPLRAVLASPCVATVITLDDHAGITFECDTH 540
OY 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595
DB 541 VESISGVMEVKYLRTSGARGTVIVPRTVEGTAKGGGEFEDTYGELERKNDTV 595

RESULT 3
O9EPUB PRELIMINARY: PRT: 595 AA.
AC O9EPUB: 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sodium/calcium exchanger 3 (Fragment).
GN SLC8A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sokolow S.; Hercheulz A.; Schurmann S.;
RT "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321404; AAC42826.2; -.
DR GDB; MGI:107976; Slc8a3.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Ext.
DR InterPro: IPR004836; NaCa_Ext.
DR Pfam; PF03160; Calx_beta; 2.
DR Pfam; PF01699; NaCa_Ext; 1.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR NON_TER 595
SQ SEQUENCE 595 AA; 66200 MW; 8EF81CBCEDB7854 CRC64;
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Query Match 93.3%; Score 3012; DB 11; Length 595;  
Best Local Similarity 97.5%; Pred. No. 6,4e-236;  
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAMLRLOPLTSAPLHFGVLTFLNLGRABAGSGDVPSTGQNNESCSSGSDCKEYIL 60  
Db 1 MAMLRLOPLTSAPLHFGVLTFLNLGRABAGSGDVPSTGQNNESCSSGSDCKEYIL 60  
QY 61 PIWPEPNSLDKLTARIVYFVALIYMLGSIITADRFMAIEVITTSOREVYTIKKPGE 120  
Db 61 PIWPEPNSLDKLTARIVYFVALIYMLGSIITADRFMAIEVITTSOREVYTIKKPGE 120  
QY 121 TSTTIRWNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIYGSAAFNFI 180  
Db 121 TSTTIRWNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIYGSAAFNFI 180  
QY 181 IIGICVYVIPDGETRKIKHLRVFTTAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240  
Db 181 IIGICVYVIPDGETRKIKHLRVFTTAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240  
QY 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMNSHFLDGN 300  
Db 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMNSHFLDGN 300  
QY 301 LVPLEGEKVEDSRREMIIRILDKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360  
Db 301 LVPLEGEKVEDSRREMIIRILDKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360  
QY 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEBEDFISKVFPPCSCYQCLNCGAVLLTYVR 420  
Db 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEBEDFISKVFPPCSCYQCLNCGAVLLTYVR 420  
QY 421 KGDMSKTMVYDYKTEDGSANAGADYEETEGTVLKPGETOKESVGIIDDDIFEDEHNF 480  
Db 421 KGDMSKTMVYDYKTEDGSANAGADYEETEGTVLKPGETOKESVGIIDDDIFEDEHNF 480  
QY 481 FVRLSNVRIEEQPEEGMPAIFNSLPPLRAVLASPCVATVYTIIDDDHAGIIFTECDTIH 540  
Db 481 FVRLSNVRIEEQPEEGMPAIFNSLPPLRAVLASPCVATVYTIIDDDHAGIIFTECDTIH 540  
QY 541 VSESIGVMEVKVLTSGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595  
Db 541 VSESIGVMEVKVLTSGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595

RESULT 4  
Q8VHJ8 PRELIMINARY; PRT; 928 AA.

AC Q8VHJ8  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Sodium/calcium exchanger.  
GN SLC8A3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=SKLEETAL MUSCLE;  
RA Kirev A.;  
RT "Towards complete inventory of calcium transporters of the house mouse.";  
RL Submitted (NCV-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF453257; ALU39160.1; -.  
DR MGD: MGI:107976; SLC8A3.  
DR InterPro: IPR003644; Calx.beta.  
DR InterPro: IPR004837; NaCa\_Exmemb.  
DR InterPro: IPR004836; Na\_Ca\_Ex.  
DR Pfam: PF01699; Na\_Ca\_Ex; 2.  
DR Pfam: PF01699; Na\_Ca\_Ex; 2.  
DR PRINTS: PRO1259; NACAEKXCHNR.

DR SMART: SM00237; Calx.beta; 2.  
DR TIGRfams: TIGR00845; caca; 1.  
SO SEQUENCE 928 AA; 102943 MW; A36BBB30BE4123C0 CRC64;

Query Match 93.3%; Score 3012; DB 11; Length 928;  
Best Local Similarity 97.5%; Pred. No. 1.2e-235;  
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 MAMLRLOPLTSAPLHFGVLTFLNLGRABAGSGDVPSTGQNNESCSSGSDCKEYIL 60  
Db 1 MAMLRLOPLTSAPLHFGVLTFLNLGRABAGSGDVPSTGQNNESCSSGSDCKEYIL 60  
QY 61 PIWPEPNSLDKLTARIVYFVALIYMLGSIITADRFMAIEVITTSOREVYTIKKPGE 120  
Db 61 PIWPEPNSLDKLTARIVYFVALIYMLGSIITADRFMAIEVITTSOREVYTIKKPGE 120  
QY 121 TSTTIRWNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIYGSAAFNFI 180  
Db 121 TSTTIRWNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIYGSAAFNFI 180  
QY 181 IIGICVYVIPDGETRKIKHLRVFTTAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240  
Db 181 IIGICVYVIPDGETRKIKHLRVFTTAAWSIFAYIMLYMLAVSPGVQVWEGILLTLFF 240  
QY 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMNSHFLDGN 300  
Db 241 FPVCVLLAMVADKRLFLFYKMKKRYRTDKHKGIIETEGDHPKGIEMDGKMNSHFLDGN 300  
QY 301 LVPLEGEKVEDSRREMIIRILDKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360  
Db 301 LVPLEGEKVEDSRREMIIRILDKOKHPEKDLDOLEVANYYALSHOOKSRAFYRIQATR 360  
QY 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEBEDFISKVFPPCSCYQCLNCGAVLLTYVR 420  
Db 361 MMTGAGNITLKKHAAEQAKKASSMSEVHTDEBEDFISKVFPPCSCYQCLNCGAVLLTYVR 420  
QY 421 KGDMSKTMVYDYKTEDGSANAGADYEETEGTVLKPGETOKESVGIIDDDIFEDEHNF 480  
Db 421 KGDMSKTMVYDYKTEDGSANAGADYEETEGTVLKPGETOKESVGIIDDDIFEDEHNF 480  
QY 481 FVRLSNVRIEEQPEEGMPAIFNSLPPLRAVLASPCVATVYTIIDDDHAGIIFTECDTIH 540  
Db 481 FVRLSNVRIEEQPEEGMPAIFNSLPPLRAVLASPCVATVYTIIDDDHAGIIFTECDTIH 540  
QY 541 VSESIGVMEVKVLTSGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595  
Db 541 VSESIGVMEVKVLTSGARGTVIYVFPRTVEGTAKGGEDFEDYGELEFKNDETV 595

RESULT 5  
O97801 PRELIMINARY; PRT; 934 AA.

AC O97801  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Sodium/calcium exchanger Isoform NCX1.3.  
GN NCX1.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
ON NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY;  
RX MEDLINE=99175198; PubMed=10075718;  
RA Li X.F., Lytton J.;  
RT "A circularized sodium-calcium exchanger exon 2 transcript.";  
RL J. Biol. Chem. 274:8153-8160(1999).  
DR EMBL: AF107593; AAD04173.1; -.  
DR InterPro: IPR003644; Calx.beta.  
DR InterPro: IPR001623; DnaJ\_N.

DR InterPro; IPR004837; NaCa\_Extremb.  
 DR InterPro; IPR004836; Na\_Ca\_Ex.  
 DR Pfam; PF03160; Calx-beta; 2.  
 DR Pfam; PF01699; Na\_Ca\_Ex; 2.  
 DR PRINTS; PR01259; NACAEXCHNGR.  
 DR SMART; SM00237; Calx\_beta; 2.  
 DR TIGRFAMs; TIGR00845; caca; 1.  
 DR PROSITE; PSS0076; DNAL; 2; 1.  
 SO SEQUENCE 934 AA; 104331 MW; 2A28DA30254ABC2 CRC64;

Query Match 66.8%; Score 2157; DB 6; Length 934;  
 Best Local Similarity 68.7%; Pred. No. 3, 5e-166;

Matches 426; Conservative 76; Mismatches 90; Indels 28; Gaps 9;

1 MAMRLQPTSAFLHGLTVFLF--LNGLRAGSGSDVPSTGONNCGSSGSDCKEGY 58  
 1 MRLSLSPFSGHFLVYVALLFSHVVDVIAETEMEGCNETGE---CTGSYCKKVV 56  
 59 ILPIWPEPNSLGDKIARVYVVALIYMFGLVSIADRPMASIEVITSQEREVTIKRN 118  
 57 ILPIWPEPNSLGDKIARVYVVALIYMFGLVSIADRPMASIEVITSQEREVTIKRN 116  
 119 GETSTTIVNWNVTNLTLMALGSSAPELLISLIVCGHGLTAGDGLSTYVGSAAFM 178  
 117 GETTQTVRIWNETVSNLTLMALGSSAPELLISLIVCGHGLTAGDGLSTYVGSAAFM 176  
 179 FLIIGICVVPIDGERTKHLRVFFITAMSIFFAYIMLYMILAVSPGVQWEGLLTL 238  
 177 FLIILACVVPIDGERTKHLRVFFITAMSIFFAYIMLYMILAVSPGVQWEGLLTL 236  
 239 FFFPVCVLLAWADKRLFYKYMKKYPTDKHRCIITETGHPKG---IEMDKMNSH 295  
 237 FFFPVCVLLAWADKRLFYKYMKKYPTDKHRCIITETGHPKG---IEMDKMNSH 296  
 296 ---FLDGNLVPLEKGVYD---ESREMTIRILDKOKHPEKLDOLVEMANYALASHO 348  
 297 VENFLDGLV-LEVDREDDDEBARREKARILKOKHPEKLDOLVEMANYALASHO 355  
 349 KSRAFYRIQATRMKAGNLIKKAHAQAOKKASMSSEVHTDEPE-DFISKVEFDPSCSYOC 407  
 356 KSRAFYRIQATRMKAGNLIKKAHAQAOKKASMSSEVHTDEPE-DFISKVEFDPSCSYOC 415  
 408 LENCAGVLLTVYRKGGDMKTYVYKTTEDGSANAGADYEFTEGIVYVLRPGEQKFSVG 467  
 416 LENCAGVLLTVYRKGGDMKTYVYKTTEDGSANAGADYEFTEGIVYVLRPGEQKFSVG 475  
 468 IIDDIFEEDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVTLDD 527  
 476 IIDDIFEEDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVTLDD 532  
 528 HAGIFTECDTHVSEISIGVMEYKVLRTSGARGTVLPFRVETGAKGGEDFEDTYGEL 587  
 533 HAGIFTECDTHVSEISIGVMEYKVLRTSGARGTVLPFRVETGAKGGEDFEDTYGEL 592  
 588 EFKNDFTV-----CDROE 600  
 593 EFKNDFTV-----CDROE 612

RESULT 6

Q28662 PRELIMINARY; PRT; 941 AA.

AC Q28662;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Renal Na/Ca exchanger NACA-2.  
 GN NCA1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_taxonomy:9986;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=92321271; PubMed=1621815;  
 RA Rellly R.F., Shugrue C.A.;  
 RT "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";  
 RL Am. J. Physiol. 262:F1105-F1109(1992).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RA Rellly R.F., Shugrue C.A.;

Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.

DR EMBL; U52665; AAA97928.1;  
 DR InterPro; IPR003644; Calx\_beta.  
 DR InterPro; IPR001623; DNAL\_N.  
 DR InterPro; IPR004837; NaCa\_Extremb.  
 DR InterPro; IPR004836; Na\_Ca\_Ex.  
 DR Pfam; PF03160; Calx-beta; 2.  
 DR Pfam; PF01699; Na\_Ca\_Ex; 2.  
 DR PRINTS; PR01259; NACAEXCHNGR.  
 DR SMART; SM00237; Calx\_beta; 2.  
 DR TIGRFAMs; TIGR00845; caca; 1.  
 DR PROSITE; PSS0076; DNAL; 2; 1.  
 SO SEQUENCE 941 AA; 105128 MW; 7E11396DE70A4084 CRC64;

Query Match 66.8%; Score 2156.5; DB 6; Length 941;  
 Best Local Similarity 68.8%; Pred. No. 3, 9e-166;

Matches 421; Conservative 77; Mismatches 87; Indels 27; Gaps 9;

8 PLTSAFLHGLTVFLF--LNGLRAGSGSDVPSTGONNCGSSGSDCKEGYILPTWPE 66  
 9 PLSMGLHLLAIVLFFFRDHWSAETEMEGCNETGE---CTGSYCKKGYILPTWPEQ 64  
 67 NSLSGDKIARVYVVALIYMFGLVSIADRPMASIEVITSQEREVTIKRNGESTTTI 126  
 65 DSGFGKIRATVYVFAVAMVYMFGLVSIADRPMASIEVITSQEREVTIKRNGESTTTI 124  
 127 RWNNEVSNLTLMALGSSAPELLISLIVCGHGLTAGDGLSTYVGSAAFMFIITGIV 186  
 125 RWNNEVSNLTLMALGSSAPELLISLIVCGHGLTAGDGLSTYVGSAAFMFIITGIV 184  
 187 YVLDGETKIRKHLRVFFITAMSIFFAYIMLYMILAVSPGVQWEGLLTFEPPVCV 246  
 185 YVLDGETKIRKHLRVFFITAMSIFFAYIMLYMILAVSPGVQWEGLLTFEPPVCV 244  
 247 LAMVADKRLFYKYMKKYPTDKHRCIITETGHPKG---IEMDKMNSH---FLDGN 300  
 245 LAMVADKRLFYKYMKKYPTDKHRCIITETGHPKG---IEMDKMNSH---FLDGN 304  
 301 LVPLEKGVYD---ESREMTIRILDKOKHPEKLDOLVEMANYALASHOKSRAFYRI 356  
 305 LV-LVDREDDDEBARREKARILKOKHPEKLDOLVEMANYALASHOKSRAFYRI 363  
 357 OATRMKAGNLIKKAHAQAOKKASMSSEVHTDEPE-DFISKVEFDPSCSYOCLENGAVL 415  
 364 OATRMKAGNLIKKAHAQAOKKASMSSEVHTDEPE-DFISKVEFDPSCSYOCLENGAVL 423  
 416 LTVYRKGGDMKTYVYKTTEDGSANAGADYEFTEGIVYVLRPGEQKFSVGIIIDDIFE 475  
 424 LTVYRKGGDMKTYVYKTTEDGSANAGADYEFTEGIVYVLRPGEQKFSVGIIIDDIFE 483  
 476 EDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVTLDDHAGIFTE 535  
 484 EDEHFEVRLSNVRIEEOPEEGMPAIFNSLPLRAVLASPCVATVTLDDHAGIFTE 540  
 536 CDTIHVSEISIGVMEYKVLRTSGARGTVLPFRVETGAKGGEDFEDTYGELFKNDFTV 595  
 541 EKVTHVSEISIGVMEYKVLRTSGARGTVLPFRVETGAKGGEDFEDTYGELFKNDFTV 600  
 596 -----CDROE 600  
 601 KTTIRIFDREE 612

## RESULT 7

ID Q9TV05 PRELIMINARY: PRT: 602 AA.

AC Q9TV05; 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Sodium-calcium exchanger circular exon 2 transcript.

CN NCX1.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY;

RX MEDLINE=99175198; PubMed=10075718;

LA L1 X.F., Lytton J.;

RL J. Biol. Chem. 274:8153-8160(1999).

DR EMBL; AF109888; AAD04174.1; -

DR InterPro: IPR003644; Calx\_beta.

DR InterPro: IPR001623; DnaJ\_N.

DR InterPro: IPR004837; NACA\_Exmemb.

DR InterPro: IPR004836; Na\_Ca\_Ex.

DR Pfam; PF03160; Calx\_beta; 2.

DR Pfam; PF01699; Na\_Ca\_Ex; 1.

DR SMART; SM00237; Calx\_beta; 2.

DR TIGRFAMs; TIGR00845; caca; 1.

DR PROSITE; PS50076; DnaJ\_2; 1.

SQ SEQUENCE 602 AA; 67369 MW; F46C6D80D1D32040E CRC64;

Query Match 66.7%; Score 2154.5; DB 6; Length 602;

Best Local Similarity 69.6%; Pred. No. 2.9e-166;

Matches 423; Conservative 75; Mismatches 89; Indels 21; Gaps 8;

QY 1 MAMLELOPLTSAFLHFGVLTFLF--LNGLRAGSGDVPSTGQNNESGSSDCKEYV 58  
DB 1 MRLSLSPFSKGFHLVLYVALFESHVDVLAETEMEGENETGE---CTGSYYCKKGV 56  
QY 59 ILPIWYPPNPISLGDRIARYVYFVALIYMFGLGVSIIADRFNASIFVITSOEREVTIKPN 118  
DB 57 ILPIWEPQDSFGDKIARYVYFVALIYMFGLGVSIIADRFNASIFVITSOEREVTIKPN 116  
QY 119 GETSTTTIRWNETVSNLTALMGSSAPETLLSLIEVCGHGFIAQDLGPSTIVGSAAFNM 178  
DB 117 GETTKTIVRIMNETVSNLTALMGSSAPETLLSLIEVCGHGFIAQDLGPSTIVGSAAFNM 176  
QY 179 FIITGICVYVPDGETRKIKHLRFVETIAWMSIFAYIMLYMLAVFSPGVQVWEGGLTL 238  
DB 177 FIILACVYVVPDGETRKIKHLRFVETIAWMSIFAYIMLYMLAVFSPGVQVWEGGLTL 236  
QY 239 FEFPYCVLAWYADRLLFYKYMKHKKRTDKHGGIIETEGDHPKG---IEMDGKMMNSH 295  
DB 237 FEFPICVYFAWYADRLLFYKYMKHKKRTDKHGGIIETEGDHPKG---IEMDGKMMNSH 296  
QY 236 ---FLDGLNVLPEKGEVD---ESRREMIRILDKOKHPEKDLQVLEMANYYALSHOO 348  
DB 237 VENFDLGLVY-LEVDERDODDEARREMARILKEKOKHPEKDLQVLEMANYYALSHOO 355  
QY 349 KSRAFYRQATFTMTGAGILKKHAAEOAKKASSMEVYTDPE--DITSKVFEDDCSYOC 407  
DB 336 KSRAFYRQATFTMTGAGILKKHAAEOAKKASSMEVYTDPE--DITSKVFEDDCSYOC 415  
QY 408 LENCAGVLLTVVRKGDMSKTYVDYKTEGDSANAGADYEFTGTVVLKPGCTOKESYVG 467  
DB 416 LENCAGVLLTVVRKGDMSKTYVDYKTEGDSANAGADYEFTGTVVLKPGCTOKESYVG 475  
QY 468 IIDDIFEDDEHFVRLSNVRIEEDQPEEGMPALFNSLPLRAVLASPCVATVITLDD 527  
DB 476 IIDDIFEDDEHFVRLSNVRIEEDQPEEGMPALFNSLPLRAVLASPCVATVITLDD 532

## RESULT 8

ID Q9TS14 PRELIMINARY: PRT: 941 AA.

AC Q9TS14; 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE NA/CA exchanger isoform NACA6.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94148976; PubMed=8106495;

LA Kofuji P., Lederer W.J., Schuitze D.H.;

RT "Mutually exclusive and cassette exons underlie alternatively spliced isoforms of the Na/CA exchanger."

J. Biol. Chem. 269:5145-5149(1994).

DR InterPro: IPR003644; Calx\_beta.

DR InterPro: IPR001623; DnaJ\_N.

DR InterPro: IPR004837; NACA\_Exmemb.

DR InterPro: IPR004836; Na\_Ca\_Ex.

DR Pfam; PF03160; Calx\_beta; 2.

DR Pfam; PF01699; Na\_Ca\_Ex; 2.

DR PRINTS; PR01259; NACAEXCHNGR.

DR SMART; SM00237; Calx\_beta; 2.

DR TIGRFAMs; TIGR00845; caca; 1.

DR PROSITE; PS50076; DnaJ\_2; 1.

SQ SEQUENCE 941 AA; 104995 MW; AEC76774E9E81815 CRC64;

Query Match 66.2%; Score 2136.5; DB 6; Length 941;

Best Local Similarity 69.5%; Pred. No. 1.6e-164;

Matches 417; Conservative 76; Mismatches 86; Indels 21; Gaps 9;

QY 8 PLTSAFLHFGVLTFLF--LNGLRAGSGDVPSTGQNNESGSSDCKEYILPIWPE 66  
DB 9 PFSMGFHLAIYLFEPFRDHYSAETEMEGENETGE---CTGSYYCKKGVILPIWPE 64  
QY 67 NPSLDKIRARYVYFVALIYMFGLGVSIIADRFNASIFVITSOEREVTIKPGETSTTI 126  
DB 65 DPSFGDKIARYVYFVALIYMFGLGVSIIADRFNASIFVITSOEREVTIKPGETSTTI 123  
QY 127 RVWNETVSNLTALMGSSAPETLLSLIEVCGHGFIAQDLGPSTIVGSAAFNMFIIGLCV 186  
DB 124 RVWNETVSNLTALMGSSAPETLLSLIEVCGHGFIAQDLGPSTIVGSAAFNMFIIGLCV 183  
QY 187 YIIPGGETRKIKHLRFVETIAWMSIFAYIMLYMLAVFSPGVQVWEGGLTLFFPVCYL 246  
DB 184 YIIPGGETRKIKHLRFVETIAWMSIFAYIMLYMLAVFSPGVQVWEGGLTLFFPVCYL 243  
QY 247 LAMVADRLLFYKYMKHKKRTDKHGGIIETEGDHPKG---TEMGKMMNSH---FLDGN 300  
DB 244 LAMVADRLLFYKYMKHKKRTDKHGGIIETEGDHPKG---TEMGKMMNSH---FLDGN 303  
QY 301 LVLPEKGEVD---ESRREMIRILDKOKHPEKDLQVLEMANYYALSHOOKSRAFYRI 356  
DB 304 LV-LVDERDODDEARREMARILKEKOKHPEKDLQVLEMANYYALSHOOKSRAFYRI 362  
QY 357 QATRMATGAGILKKHAAEOAKKASSMEVYTDPE--DITSKVFEDPCYQCLBNCAGVL 415  
DB 363 QATRMATGAGILKKHAAEOAKKASSMEVYTDPE--DITSKVFEDPCYQCLBNCAGVL 422  
QY 416 LTVVRKGDMSKTYVDYKTEGDSANAGADYEFTGTVVLKPGCTOKESYVGIIDDIRE 475

Dd		423	LTIIRRGDGLTIVTVYDFEDFTEDEGTAGNAGSDIYETEGTVVFKGCEFOKEIRNGIIDDIDE	482
Oy		476	EDEHFEVLRSNVRIEEOPEEGMPAIFNSLPLPRAVLASPCVATVTILDDHAGITFEE	535
Dd		483	EDENFLVHSNKVKVSSETSEDGILEANHRS--TLACIASPCTAFATVIIPDDDHAGITFEE	539
Oy		536	COTIVSESIGVMWEKVLRTSGARGVITYPFRTVEGTAKGGGEDEDPTIGELEFKNDIEV	595
Dd		540	ESVTVHVESIGIMEWKVLTSGARGVNIVPYKTIEGTANGGEDFDTCGELEFONDEIV	599
		RESULT 9		
		O9R238	PRELIMINARY:	PRT: 934 AA.
ID		O9R238		
AC		O9R238:		
DT		01-MAY-2000 (TREMBLrel. 13, Created)		
DT		01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT		01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE		Na+/Ca <sup>2+</sup> -exchanging protein.		
OS		Rattus norvegicus (Rat).		
DE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
DE		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX		NCBI_Taxid=10116;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		STRAIN-DABL/RAP R SPRAGUE-DAWLEY;		
RA		Unlap M.T., Bell P.D.;		
RT		"CDNA cloning of two Na/Ca <sup>2+</sup> exchangers in mesangial cells from Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."		
RL		Submitted (Nov-1998) to the EMBL/Genbank/DBJ databases.		
DR		EMBL, AF109163; AAD23386.1; -.		
DR		InterPro: IPR003644; Calx_beta.		
DR		InterPro: IPR001623; DnaJ_N.		
DR		InterPro: IPR004837; NaCa_Exmemb.		
DR		InterPro: IPR004836; Na_Ca_Ex.		
DR		Pfam: PF03160; Calx-beta; 2.		
DR		Pfam: PF01699; Na_Ca_Ex; 2.		
DR		PRINTS: PR01259; MACAECHNGR.		
DR		SMART: SM00237; Calx_beta; 2.		
DR		TIGRFAMs: TIGR00845; caca; 1.		
DR		PROSITE: PS50076; DNAL2; 1.		
SQ		SEQUENCE 934 AA: 104166 MW: C04EDD8A75633DDC CRC64:		
		Query Match	66.1%; Score 2133; DB 11; Length 934;	
		Best Local Similarity	67.9%; Pred. No. 3.1e-164;	
		Matches 424; Conservative 72; Mismatches 88; Indels 40; Gaps 10,		
Oy		4	LRLQLTSALFHFGLVTFVLF-----NCLRRAAGSGSDVPSTGCNNCGSSGSDDCK	55
		2	LRLSPPNVSNMGRFLVTLVALFTTHVDHTADTEATGEN-----ETTCTGTSYCK	53
Oy		56	EGVILPIWPEKPSLGDKTARIVYFVALIYMEFGISITADRFMASIEYTSOEREWTK	115
Dd		54	KGVILPIWPEKPSLGDKTARIVYFVALIYMEFGISITADRFMASIEYTSOEREWTK	113
Oy		116	KPNGESTTTIRWMNETYSNLTLMAIGSSAPEILLSLIEVCSHGFIAGDLGSTIVGSA	175
Dd		114	KPNGESTTTIRWMNETYSNLTLMAIGSSAPEILLSLIEVCCHNFPAGDLGSTIVGSA	173
Oy		176	FNMFTIIIGCVVIVDGETRKIKHLRVFFITAAWSIFATIMLMLANFSPCVVOYMESL	235
Dd		174	FNMFTIIIGCVVIVDGETRKIKHLRVFFITAAWSIFATIMLMLANFSPCVVMEWEL	233
Oy		236	LTLFFEPVCVLLAWAADKRLIFYKKMHKKYPTDKHGIIIEHGHKPG--IENDGMKM	292
Dd		234	LTLFFEPICVFAMWADRLLFTKYIKRYRGKGKMGKIIEHGHDPASKTEIENDGMKV	293
Oy		293	NSH---FLDGNLVPLEGKVD---ESRRKMTIRLIKLDKOKRPERKDLOLVMANUYALS	345
Dd		294	NSHVNDPLDGALV-LVEDRDODDDEAREMARILIKELKOKRPMDEIDELLILANYOLS	352
Oy		346	HQKRATRYTRIDATRMNTGAGNILKKHAEAOKKASSSEVHTDEP-DLISKVFPPDCS	404

DB	Accession	Gene	Protein	Length	Score	DB 11	Length 934	DB 12	Score	DB 13	Length 934	DB 14	Score	DB 15	Length 934	DB 16	Score	DB 17	Length 934	DB 18	Score	DB 19	Length 934	DB 20	Score	DB 21	Length 934	DB 22	Score	DB 23	Length 934	DB 24	Score	DB 25	Length 934	DB 26	Score	DB 27	Length 934	DB 28	Score	DB 29	Length 934	DB 30	Score	DB 31	Length 934	DB 32	Score	DB 33	Length 934	DB 34	Score	DB 35	Length 934	DB 36	Score	DB 37	Length 934	DB 38	Score	DB 39	Length 934	DB 40	Score	DB 41	Length 934	DB 42	Score	DB 43	Length 934	DB 44	Score	DB 45	Length 934	DB 46	Score	DB 47	Length 934	DB 48	Score	DB 49	Length 934	DB 50	Score	DB 51	Length 934	DB 52	Score	DB 53	Length 934	DB 54	Score	DB 55	Length 934	DB 56	Score	DB 57	Length 934	DB 58	Score	DB 59	Length 934	DB 60	Score	DB 61	Length 934	DB 62	Score	DB 63	Length 934	DB 64	Score	DB 65	Length 934	DB 66	Score	DB 67	Length 934	DB 68	Score	DB 69	Length 934	DB 70	Score	DB 71	Length 934	DB 72	Score	DB 73	Length 934	DB 74	Score	DB 75	Length 934	DB 76	Score	DB 77	Length 934	DB 78	Score	DB 79	Length 934	DB 80	Score	DB 81	Length 934	DB 82	Score	DB 83	Length 934	DB 84	Score	DB 85	Length 934	DB 86	Score	DB 87	Length 934	DB 88	Score	DB 89	Length 934	DB 90	Score	DB 91	Length 934	DB 92	Score	DB 93	Length 934	DB 94	Score	DB 95	Length 934	DB 96	Score	DB 97	Length 934	DB 98	Score	DB 99	Length 934	DB 100	Score	DB 101	Length 934	DB 102	Score	DB 103	Length 934	DB 104	Score	DB 105	Length 934	DB 106	Score	DB 107	Length 934	DB 108	Score	DB 109	Length 934	DB 110	Score	DB 111	Length 934	DB 112	Score	DB 113	Length 934	DB 114	Score	DB 115	Length 934	DB 116	Score	DB 117	Length 934	DB 118	Score	DB 119	Length 934	DB 120	Score	DB 121	Length 934	DB 122	Score	DB 123	Length 934	DB 124	Score	DB 125	Length 934	DB 126	Score	DB 127	Length 934	DB 128	Score	DB 129	Length 934	DB 130	Score	DB 131	Length 934	DB 132	Score	DB 133	Length 934	DB 134	Score	DB 135	Length 934	DB 136	Score	DB 137	Length 934	DB 138	Score	DB 139	Length 934	DB 140	Score	DB 141	Length 934	DB 142	Score	DB 143	Length 934	DB 144	Score	DB 145	Length 934	DB 146	Score	DB 147	Length 934	DB 148	Score	DB 149	Length 934	DB 150	Score	DB 151	Length 934	DB 152	Score	DB 153	Length 934	DB 154	Score	DB 155	Length 934	DB 156	Score	DB 157	Length 934	DB 158	Score	DB 159	Length 934	DB 160	Score	DB 161	Length 934	DB 162	Score	DB 163	Length 934	DB 164	Score	DB 165	Length 934	DB 166	Score	DB 167	Length 934	DB 168	Score	DB 169	Length 934	DB 170	Score	DB 171	Length 934	DB 172	Score	DB 173	Length 934	DB 174	Score	DB 175	Length 934	DB 176	Score	DB 177	Length 934	DB 178	Score	DB 179	Length 934	DB 180	Score	DB 181	Length 934	DB 182	Score	DB 183	Length 934	DB 184	Score	DB 185	Length 934	DB 186	Score	DB 187	Length 934	DB 188	Score	DB 189	Length 934	DB 190	Score	DB 191	Length 934	DB 192	Score	DB 193	Length 934	DB 194	Score	DB 195	Length 934	DB 196	Score	DB 197	Length 934	DB 198	Score	DB 199	Length 934	DB 200	Score	DB 201	Length 934	DB 202	Score	DB 203	Length 934	DB 204	Score	DB 205	Length 934	DB 206	Score	DB 207	Length 934	DB 208	Score	DB 209	Length 934	DB 210	Score	DB 211	Length 934	DB 212	Score	DB 213	Length 934	DB 214	Score	DB 215	Length 934	DB 216	Score	DB 217	Length 934	DB 218	Score	DB 219	Length 934	DB 220	Score	DB 221	Length 934	DB 222	Score	DB 223	Length 934	DB 224	Score	DB 225	Length 934	DB 226	Score	DB 227	Length 934	DB 228	Score	DB 229	Length 934	DB 230	Score	DB 231	Length 934	DB 232	Score	DB 233	Length 934	DB 234	Score	DB 235	Length 934	DB 236	Score	DB 237	Length 934	DB 238	Score	DB 239	Length 934	DB 240
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Db 234 LTFEFPICVAFVAVADBRLLFEYKYVYKRYRAGKRGMIIEHGGRPASKEIEMDGKVV 293
Qy 293 NSH---FLDGLNVLPEGEVD---ESRREMIRIKDKOKHPEKDLDOLYEMANYALS 345
Db 294 NSHVNFLDGLNVL-LEVERODDDEARREMARILKELKOKHPDKEIOLIELANYOYLS 352
Qy 346 HOOKSRAFYRIOATRYMTAGNILKHAADQARKKAVSNHEVMMDVENDPVSKEVFEEDGT 404
Db 353 OOKSRAFYRIOATRYMTAGNILKHAADQARKKAVSNHEVMMDVENDPVSKEVFEEDGT 412
Qy 405 YOCLENCGAVLLTVVRKGGDMSTMYVDYKTEEDGSANAGADYEFTGTVLKPGETOKEF 464
Db 413 YOCLENCGAVLLTVVRKGGDLNTYVDFRTEEDGTANAGSDYEFTGTVIFRGETOKEI 472
Qy 465 SVGIIDDDIFEEDEHFYRLSNVRIEEOPEEGMPAIFNSLPLPR-AVLASPCVATYTI 523
Db 473 RVGIIDDDIFEEDEHFYRLSNVRSSEVEDG---ILDSNHSVAIACLSGPNATITTI 528
Qy 524 LDDHAGIFTECDTIHVSSEIGMEVYVLRSGARGVYVPERVEGTAKGGGDEEDT 583
Db 529 FDDHAGIFTEPEPTVHVSSEIGMEVYVLRSGARGVYVPERVEGTAKGGGDEEDT 588
Qy 584 YGELEFKNDETV-----CDROE 600
Db 589 CGELEFONDEIVKITTIRIFREE 612

RESULT 11
Qy 939239 PRELIMINARY: PRT: 957 AA.
Qy 939239
AC 09R239;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Na+/Ca2+-exchanging protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DAHL/RAPP S SPRAGUE-DAWLEY;
RA Unlap M.T., Bell P.D.;
RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.
EMBL: AF109164; AAD23387.1;
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ex; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PS50076; DNaJ_2; 1.
SQ SEQUENCE 957 AA; 106724 MW; 7A1A6630451EAA7E CRC64;

Query Match 66.0%; Score 2129; DB 11; Length 957;
Best Local Similarity 67.8%; Pred. No. 6.8e-164;
Matches 423; Conservative 72; Mismatches 89; Indels 40; Gaps 10;

Qy 4 LRLDPLTSAPLHGLVTVFLP-----NGLRAAGSGSDVPSTGONNESCSSSDCK 55
Db 2 LRLSLPPLVNSMGFRLVTLVALLFTVHDHTADTAEATGSGN-----ETTECTGTSYCK 53
Qy 56 EGVVPIYTPPEPSLGDVIARIYVVALITYFLGVSTIADRFMASIEYTSQEREVITK 115
Db 54 KGVIIPIPEPDPSPGDIARIATVFAVMYFLGVSTIADRFMSIEYTSQEREVITK 113
Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSTLIEVCGHPTAGDLSGTIVGSA 175

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Db 114 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSTLIEVCGHNTADDLGPTIVGSA 173
Qy 176 FNMFTIIGICVYVPDGETRKIKHLRVEFTPAANSIFAYIMLYMLAVSPGCVNOVWGL 235
Db 174 FNMFTIILCVYVPDGETRKIKHLRVEFTPAANSIFAYIMLYMLAVSPGCVNOVWGL 233
Qy 236 LTFEFPICVLLAVADBRLLFEYKYVYKRYRAGKRGMIIEHGGRPASKEIEMDGKVV 292
Db 234 LTFEFPICVAVAVADBRLLFEYKYVYKRYRAGKRGMIIEHGGRPASKEIEMDGKVV 293
Qy 293 NSH---FLDGLNVLPEGEVD---ESRREMIRIKDKOKHPEKDLDOLYEMANYALS 345
Db 294 NSHVNFLDGLNVL-LEVERODDDEARREMARILKELKOKHPDKEIOLIELANYOYLS 352
Qy 346 HOOKSRAFYRIOATRYMTAGNILKHAADQARKKAVSNHEVMMDVENDPVSKEVFEEDGT 404
Db 353 OOKSRAFYRIOATRYMTAGNILKHAADQARKKAVSNHEVMMDVENDPVSKEVFEEDGT 412
Qy 405 YOCLENCGAVLLTVVRKGGDMSTMYVDYKTEEDGSANAGADYEFTGTVLKPGETOKEF 464
Db 413 YOCLENCGAVLLTVVRKGGDLNTYVDFRTEEDGTANAGSDYEFTGTVIFRGETOKEI 472
Qy 465 SVGIIDDDIFEEDEHFYRLSNVRIEEOPEEGMPAIFNSLPLPR-AVLASPCVATYTI 523
Db 473 RVGIIDDDIFEEDEHFYRLSNVRSSEVEDG---ILDSNHSVAIACLSGPNATITTI 528
Qy 524 LDDHAGIFTECDTIHVSSEIGMEVYVLRSGARGVYVPERVEGTAKGGGDEEDT 583
Db 529 FDDHAGIFTEPEPTVHVSSEIGMEVYVLRSGARGVYVPERVEGTAKGGGDEEDT 588
Qy 584 YGELEFKNDETV-----CDROE 600
Db 589 CGELEFONDEIVKITTIRIFREE 612

RESULT 12
Qy 931237 PRELIMINARY: PRT: 600 AA.
Qy 931237
AC 091237;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sodium-calcium exchanger (Fragment).
DE SLC8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RA Koushik S.V., Conway S.J.;
RT "Role of Sodium Calcium Exchanger During Embryonic Heart
Development".
Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
EMBL: AF423306; AAL18847.1;
DR MGI: MGI:107956; Slc8a1.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR Pfam: PF03160; Calx_beta; 2.
DR Pfam: PF01699; NaCa_Ex; 1.
DR TIGRFAMs: TIGR00845; caca; 1.
DR PROSITE: PS50076; DNaJ_2; 1.
FT NON_TER 600
SQ SEQUENCE 600 AA; 66918 MW; 0307B0A126287247 CRC64;

Query Match 65.9%; Score 2128.5; DB 11; Length 600;
Best Local Similarity 68.7%; Pred. No. 3.7e-164;
Matches 414; Conservative 76; Mismatches 98; Indels 15; Gaps 6;

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OY		4	LRLDPLTASFLHFGVLTFTVLTLNGLRAAGSGGVPSPNGNESCSSSDCKEIVLPIW	63
Dd		2	LRLSLPRAWSMGFRVALVALVALLFSFVDHTIDTAETEGNGETTCTGSYYCKKVVLPIM	61
OY		64	YPENPSLDCKIARLVLYVFVALIYMFGLSVITADRFMASIEVITSQERVTIKKNGETST	123
Dd		62	EPODSFEDCDIARATAVVYEVAMVMFLGSIIADRFMSSIIEVITSQEKRTFKRPNGETJK	121
OY		124	TTRIRVNTEVSNTLTMALGSSAPELLISLEVCCHGFAGDLGGSTTVGSAAFMPFIIG	183
Dd		122	TTVRKMNTEVSNTLTMALGSSAPELLISLEVCGHNFFAGDLGGSTTVGSAAFMPFIITA	181
OY		184	ICVVVIPDGERTRIKHNLHFVEFTLAAMSIFAYITWLMLAVFSPGVQVMEGLTLTFEPV	243
Dd		182	LCVVVVPDGETRKIKHLHFVEFTVAAMSIFAFTWLIYILSVSPGVVEWGELTLFFFFPI	241
OY		244	CYLLAWADVADRKLFLPKYKKHKRYTRDKNHGIILETGDPKPC--LEMDKKMNSH--FL	297
Dd		242	CVVEFAWADVDRRLFLPKKYKKRYKRGRKGOMTIEHEGDRPASKTBIEMDGKVNSHVNFL	301
OY		298	DGNLVPLEGKEVD---ESREMRTRI.KDLKOKRPEKDLDLVEMANYALSHOOKSRAF	355
Dd		302	DGALV-LEVDERDDODEARREMARILKELKOKRPEKIEDLIBELANQVLSOQOKRAF	366
OY		354	YRIQTATRMGTAGNITLKRNAEAQAKKASSMSWEVHTDEPE-DFIKSVEFDPCSVOCLENG	412
Dd		361	YRIQTATRLMTAGNITLKRNAHADQARKAASHMEVNMEMAENDPVSKIFEEOGYOCLENG	420
OY		413	AVILLTVNRGGDMSTMYDVDTKYTDGSSNAADVEPTREGTVLTKPGEQKFYSVIIDD	472
Dd		421	TYALTINRRGGDLSTFYVDFDRTGEDGTANNAGSDYEFTGTVIFRPGETQKEIRVGIIIDD	486
OY		473	IPEEDEHFEFVRLSNVRIEEDEOPBEGMPAIRNS.LPLPAVLASCPVATVITLDDDHAGIF	532
Dd		481	IPEEDENFLVHLSNVRSVSDSEVDGEI--LESNNASSIACLGSPSTATITTFIDDDHAGIF	537
OY		533	TPEECTTHVESIGVMEKVKVLTGTSGARTVYPPRTVBGTAKKGGCEPDFTYGLSEKND	592
Dd		538	TPEEPVTVHVSIGIMEVKVLTGTSGARGNVIIIPYKTIEGTARGGEGDEFDTCGLERFOND	597
OY		593	ETV 595	
Dd		598	ETV 600	
<hr/>				
RESULT 13				
O9ET74		O9ET74	PRELIMINARY;	PRT; 600 AA.
AC		O9ET74;		
RC		01-MAR-2001 (TREMBLrel. 16, Created)		
RX		01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
RA		01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE		Na/Ca exchanger (Fragment).		
GN		SIC8A1.		
OC		Mus musculus (Mouse).		
CC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
NCBI_TaxId=10090;		Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.		
RA		Nabeshima Y.;		
RT		"Isolation and characterization of Na(+)/Ca(2+) exchanger gene and		
RL		splicing isoforms in mice."		
DR		EMBL; AB030885; BAB08169.1; -.		
DR		MGI; MGI:107956; Slc8a1.		
DR		InterPro; IPR003644; Calx.beta.		
DR		InterPro; IPR001623; DnaJ_N.		
DR		InterPro; IPR004837; NaCa_Exmemb.		
DR		InterPro; IPR004836; Na_Ca_Ex.		

[illegible]



"Cloning and expression of a mesangial cell Na<sup>+</sup>/Ca<sup>2+</sup> exchanger from  
RT Sprague-Dawley rats."  
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF033398; AAK52307.1; -  
DR InterPro: IPR003644; Calx\_beta.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR004837; NaCa\_Exmemb.  
DR InterPro: IPR004836; NaCa\_Ex.  
DR Pfam: PF03160; Calx\_beta; 2.  
DR Pfam: PF01699; NaCa\_Ex; 2.  
DR TIGRfams: TIGR00845; caca; 1.  
DR PROSITE: PS50076; DnaJ\_2; 1.  
SQ SEQUENCE 962 AA; 107270 MW; 1AA42ED25964182 CRC64;  
Query Match 65.8%; Score 2124; DB 11; Length 962;  
Best Local Similarity 67.6%; Pred. No. 1.8e-163;  
Matches 422; Conservative 73; Mismatches 89; Indels 40; Gaps 10;  
4 LRLQPLTSAFLHFGVLTFTVFL-----NGLRAEAGSGDVPSTGQNNESCGSSSDCK 55  
2 LRLSLPPVNSMGFRLVTLVALLFTVHDITADTEAETGNN-----ETTECTGTSYCK 53  
56 EGVLLPIWYPENPSLGDRIARIYVEVALIYMFGLVSIADRFMASEIVTSQEREVTIK 115  
54 KGVLLPIWEPQDPSFGDKIARATYVFVAMVYFGLVSIADRFMSIEIVTSQEREVTIK 113  
116 KPNGETSTTIRVWNETYSNLTLMALGSSAPEILSLIEVCGHGFIADLGPSTIVGSA 175  
114 KPNGETTITVIRVWNETYSNLTLMALGSSAPEILSPVIEVCGHNTAGDLGPSTIVGSA 173  
176 FNMFIITIGICVYVTPDGETRTRIKHLRVFFITAAWSIFAYIMLYMLVAFSPGVVWVWGL 235  
174 FNMFIITLVCYVVPDGETRTRIKHLRVFFITAAWSIFAYIMLYMLVAFSPGVVWVWGL 233  
236 LTFEFPVCLLAWADRLFLFYKYMHRKRTDKRGIIIEEGDHPKG---IENDGKMM 292  
234 LTFEFPICVAFVWADRLFLFYKYMHRKRTDKRGIIIEEGDHPKG---IENDGKMM 293  
293 NSH---FLDGLNVPLEGEVD---ESRREMRIRIKDKOKHPEKDLQVEMANYALS 345  
294 NSHVDNFLDGLV-LEVERDQDDDEARERARILKELKOKHPEKDLQVEMANYALS 352  
346 HQQSRARVRIQATRTMAGNILKHAADQARKVSMHEVMVDVENDPVSKEVFEEDGT 404  
353 HQQSRARVRIQATRTMAGNILKHAADQARKVSMHEVMVDVENDPVSKEVFEEDGT 412  
405 YQCLNCGAVLLTVVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVLKPGETOKEF 464  
413 YQCLNCGVALLTIRRGDLTNVFDRTEDGTANAGSDYEFTEGTVIFKPGETOKEI 472  
465 SVGIITDDIIFEDDEHFVRLSNVRIEEDQPEEGMPALFNSLPDR-AVLASPCAATYTI 523  
473 RVGIITDDIIFEDDENFLVLSNVRSVSGVSEEG---ILDSNHSVAICLSPNATITTI 528  
524 LDDHAGITFECDTIHVSIGVMEVYVLRSGARGVYVFRVVEGTAKAGGGEFEDT 583  
529 FDDDHAGITFEDEPVTHVSESIGIMEVYVLRSGARGVYVFRVVEGTAKAGGGEFEDT 588  
584 YGELEFKNDETV-----CDROE 600  
589 CGELEFONDEIVKITTIRIFDREE 612  
RESULT 15  
ID Q9WU29 PRELIMINARY; PRT; 969 AA.  
AC Q9WU29;  
DT 01-NOV-1999 (Tremblrel. 12, Created)  
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Na<sup>+</sup>/Ca<sup>2+</sup>-exchanging protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY;  
RA Unlap M.T., Bell P.D.;  
RT "cDNA cloning of two Na<sup>+</sup>/Ca<sup>2+</sup> exchangers in mesangial cells from  
RT Dahl/rapp salt-sensitive (S) and salt-resistant (R) rats."  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF109165; AAD23388.1; -  
DR InterPro: IPR003644; Calx\_beta.  
DR InterPro: IPR001623; DnaJ\_N.  
DR InterPro: IPR004837; NaCa\_Exmemb.  
DR InterPro: IPR004836; NaCa\_Ex.  
DR Pfam: PF03160; Calx\_beta; 2.  
DR Pfam: PF01699; NaCa\_Ex; 2.  
DR PRINTS: PR01259; NACAECHNGR.  
DR SMART: SM00237; Calx\_beta; 2.  
DR TIGRfams: TIGR00845; caca; 1.  
DR PROSITE: PS50076; DnaJ\_2; 1.  
SQ SEQUENCE 969 AA; 106037 MW; 1D64F6073D3C9CF5 CRC64;  
Query Match 65.8%; Score 2124; DB 11; Length 969;  
Best Local Similarity 67.6%; Pred. No. 1.8e-163;  
Matches 422; Conservative 73; Mismatches 89; Indels 40; Gaps 10;  
4 LRLQPLTSAFLHFGVLTFTVFL-----NGLRAEAGSGDVPSTGQNNESCGSSSDCK 55  
2 LRLSLPPVNSMGFRLVTLVALLFTVHDITADTEAETGNN-----ETTECTGTSYCK 53  
56 EGVLLPIWYPENPSLGDRIARIYVEVALIYMFGLVSIADRFMASEIVTSQEREVTIK 115  
54 KGVLLPIWEPQDPSFGDKIARATYVFVAMVYFGLVSIADRFMSIEIVTSQEREVTIK 113  
116 KPNGETSTTIRVWNETYSNLTLMALGSSAPEILSLIEVCGHGFIADLGPSTIVGSA 175  
114 KPNGETTITVIRVWNETYSNLTLMALGSSAPEILSPVIEVCGHNTAGDLGPSTIVGSA 173  
176 FNMFIITIGICVYVTPDGETRTRIKHLRVFFITAAWSIFAYIMLYMLVAFSPGVVWVWGL 235  
174 FNMFIITLVCYVVPDGETRTRIKHLRVFFITAAWSIFAYIMLYMLVAFSPGVVWVWGL 233  
236 LTFEFPVCLLAWADRLFLFYKYMHRKRTDKRGIIIEEGDHPKG---IENDGKMM 292  
234 LTFEFPICVAFVWADRLFLFYKYMHRKRTDKRGIIIEEGDHPKG---IENDGKMM 293  
293 NSH---FLDGLNVPLEGEVD---ESRREMRIRIKDKOKHPEKDLQVEMANYALS 345  
294 NSHVDNFLDGLV-LEVERDQDDDEARERARILKELKOKHPEKDLQVEMANYALS 352  
346 HQQSRARVRIQATRTMAGNILKHAADQARKVSMHEVMVDVENDPVSKEVFEEDGT 404  
353 HQQSRARVRIQATRTMAGNILKHAADQARKVSMHEVMVDVENDPVSKEVFEEDGT 412  
405 YQCLNCGAVLLTVVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVLKPGETOKEF 464  
413 YQCLNCGVALLTIRRGDLTNVFDRTEDGTANAGSDYEFTEGTVIFKPGETOKEI 472  
465 SVGIITDDIIFEDDEHFVRLSNVRIEEDQPEEGMPALFNSLPDR-AVLASPCAATYTI 523  
473 RVGIITDDIIFEDDENFLVLSNVRSVSGVSEEG---ILDSNHSVAICLSPNATITTI 528  
524 LDDHAGITFECDTIHVSIGVMEVYVLRSGARGVYVFRVVEGTAKAGGGEFEDT 583  
529 FDDDHAGITFEDEPVTHVSESIGIMEVYVLRSGARGVYVFRVVEGTAKAGGGEFEDT 588  
584 YGELEFKNDETV-----CDROE 600  
589 CGELEFONDEIVKITTIRIFDREE 612  
Search completed: November 30, 2002, 12:30:57  
Job time : 41.0266 secs

